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Range: from begin to end Features: ☒ CDD

☐ 1: [XP_001502439](#). Reports PREDICTED: simila...[gi:149705828]

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LOCUS XP_001502439 481 aa linear MAM 25-JUN-2007
 DEFINITION PREDICTED: similar to Hyaluronoglucosaminidase 4 [Equus caballus].
 ACCESSION XP_001502439
 VERSION XP_001502439.1 GI:149705828
 DBSOURCE REFSEQ: accession [XM_001502389.1](#)
 KEYWORDS
 SOURCE Equus caballus (horse)
 ORGANISM [Equus caballus](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Perissodactyla; Equidae; Equus.
 COMMENT MODEL [REFSEQ](#): This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW_001799716](#)) using gene prediction method: GNOMON, supported by mRNA evidence.
 Also see:
[Documentation of NCBI's Annotation Process](#)

FEATURES	Location/Qualifiers
source	1..481 /organism="Equus caballus" /isolate="Twilight" /db_xref="taxon:9796" /chromosome="4" /sex="female" /breed="thoroughbred"
Protein	1..481 /product="similar to Hyaluronoglucosaminidase 4" /calculated_mol_wt=54569
Region	41..373 /region_name="Glyco_hydro_56" /note="Hyaluronidase; pfam01630" /db_xref="CDD:89585"
CDS	1..481 /gene="LOC100056514" /coded_by="XM_001502389.1:72..1517" /db_xref="GeneID:100056514"

ORIGIN

```

1 mkl1segqfr fcvvqpihlt swlliffilk sisslkparl piyqrkpfia awnaptdqcl
61 ikynirlnlk mfqvigsp1a kargqnvtf yvnrlgyypw ytsqgvpng glpqnislqv
121 hlekadedin yyipaedfsg laavidweywr pqwarnwnk dvyrqksrkl isdmqenvsa
181 tdieylakat feesakafmk etielgiksr pkg1wggyly pdchnynvyd pnytgscpee
241 evlrnnelsw lwnssaalyp sigvrkslgd senilrfsqf rvhesmrist mtshdialpv
301 fvytrlgyrd eplfflskqd listigesaa lgaagfviwg dmnltssegn ctkvkqfvss
361 vlgrivnvt raaeacslhl crnngcr1rk vwkapydlhl npasyyieas edgefivegk

```




421 asdtldalma ekfscqcyqg yegadcremk tadgcsglps fsgslitlcp lflagyqsiq
481 1

//

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Range: from begin to end Features: ☒ CDD

☐ 1: AAC98883. Reports hyaluronidase 4 [...[gi:4090792]]

[BLink](#), [Conserved Domains](#), [Links](#)

Features Sequence

LOCUS AAC98883 481 aa linear PRI 14-OCT-1999
 DEFINITION hyaluronidase 4 [Homo sapiens].
 ACCESSION AAC98883
 VERSION AAC98883.1 GI:4090792
 DBSOURCE locus AF009010 accession AF009010.1
 KEYWORDS .
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini;
 Catarrhini; Hominidae; Homo.
 REFERENCE 1 (residues 1 to 481)
 AUTHORS Csoka,A.B., Scherer,S.W. and Stern,R.
 TITLE Expression analysis of six paralogous human hyaluronidase genes
 clustered on chromosomes 3p21 and 7q31
 JOURNAL Genomics 60 (3), 356-361 (1999)
 PUBMED 10493834
 REFERENCE 2 (residues 1 to 481)
 AUTHORS Csoka,A.B.
 TITLE Direct Submission
 JOURNAL Submitted (17-JUN-1997) Pathology, University of California,
 Parnassus at 3rd Avenue, San Francisco, CA 94143, USA
 COMMENT Method: conceptual translation supplied by author.
 FEATURES Location/Qualifiers
 source 1..481
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="7"
 /map="7q31.3"
Protein 1..481
 /product="hyaluronidase 4"
 /name="PH-20 paralog"
Region 41..373
 /region_name="Glyco_hydro_56"
 /note="Hyaluronidase; pfam01630"
 /db_xref="CDD:89585"
CDS 1..481
 /gene="HYAL4"
 /coded_by="AF009010.1:642..2087"
 /note="highest expression in placenta and skeletal muscle"
 ORIGIN
 1 mkvlsegqlk lcvvqpvhlt swlliffilk sisclkparl piyqrkpfia awnaptdqcl
 61 ikynlrlnlk mfpvigspla kargqnvtf yvnrlgyypw ytsqgvping glpqnislqv
 121 hlekadqdin yyipaedfsg laavidweywr pqwarnwnsk dvyrqksrkl isdmgknvsa



```
181 tdieylakvt feesakafmk etiklgiks r pkglwgyyly pdchnynvya pnysgscped
241 evlrnnelsw lwnssaalyp sicvwkslgd senilrfskf rvhesmrist mtshdyalpv
301 fvytrlgyrd eplfflskqd lvstigesaa lgaagiviwg dmnltaskan ctkvkqfvss
361 dlgsyianvt raaevcsllh crnngrcirk mwnapsylhl npasyhieas edgeftvkgk
421 asdtdlavma dtfschcygg yegadcreik tadgcsgvsp spgslmtlcl lllasyrsiq
481 l
```

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Exhibit C



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Range: from begin to end Features: ☒ CDD

☐ 1: [XP_001086758](#). Reports PREDICTED: simila...[gi:109068040]

[BLink](#), [Conserved Domains](#), [Links](#)

Comment Features Sequence

LOCUS XP_001086758 481 aa linear PRI 14-JUN-2006
 DEFINITION PREDICTED: similar to hyaluronoglucosaminidase 4 [Macaca mulatta].
 ACCESSION XP_001086758
 VERSION XP_001086758.1 GI:109068040
 DBSOURCE REFSEQ: accession [XM 001086758.1](#)
 KEYWORDS .
 SOURCE Macaca mulatta (rhesus monkey)
 ORGANISM [Macaca mulatta](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Cercopithecidae; Cercopithecinae; Macaca.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW 001114282](#)) using gene prediction method: GNOMON, supported by mRNA and EST evidence.
 Also see:

[Documentation of NCBI's Annotation Process](#)

FEATURES	Location/Qualifiers
source	1..481 /organism="Macaca mulatta" /isolate="17573" /db_xref="taxon:9544" /chromosome="3" /sex="female" /country="USA: Southwest National Primate Research Center at the Southwest Foundation for Biomedical Research, San Antonio, TX" /note="derived from Indian origin rhesus"
<u>Protein</u>	1..481 /product="similar to hyaluronoglucosaminidase 4" /calculated_mol_wt=54446
<u>Region</u>	41..373 /region_name="Glyco_hydro_56" /note="Hyaluronidase; pfam01630" /db_xref="CDD:89585"
<u>CDS</u>	1..481 /gene="LOC696128" /coded_by="XM_001086758.1:54..1499" /db_xref="GeneID:696128"

ORIGIN

```

1 mkvlpegqlr lcfvqpvhlt lwlliffilk sisclckparl piyqrkpfia awnaptdqcl
61 ikynlrlnlk mfpvigspla kargqnvtf yvnrlgyypw ytsqgvping glpqnislqv
121 hlekadqdin yyipdedfsg laavidweywr pqwarnwnak dvyrkksrkl itdmgknvsa
  
```



```
181 tdieylakvt feesakafmk etiklgiksr pkglwgyyly pdchnynvya pnytgscpee
241 evlrnnelsw lwnssaalyp sigvwkslgd senilrfsqf rvhesmrist mtshdialpv
301 fvytrlgyrd eplfflskqd lvstigesaa lgaagiviwg dmnltskan ctkvkqfvss
361 dlgsylanvt raaevcsfhl crnngrcirk mwnsptylhl npasyhieas edgeftvkgr
421 asdtldavma dtfschcyqg yegadcrevk tadgcsqvsp fpgslitlcl lllasyrsih
481 l
```

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Exhibit D

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Range: from to Features: ☒ CDD

☐ 1: [NP_084124](#). Reports hyaluronoglucosam...[gi:116812879]

[BLink](#), [Conserved Domains](#), [Links](#)
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LOCUS NP_084124 481 aa linear ROD 11-FEB-2008
 DEFINITION hyaluronoglucosaminidase 4 [Mus musculus].
 ACCESSION NP_084124 XP_132998 XP_917828 XP_995969
 VERSION NP_084124.1 GI:116812879
 DBSOURCE REFSEQ: accession [NM_029848.1](#)
 KEYWORDS .
 SOURCE Mus musculus (house mouse)
 ORGANISM [Mus musculus](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
 Sciurognathi; Muroidea; Muridae; Murinae; Mus.
 REFERENCE 1 (residues 1 to 481)
 AUTHORS Kim,E., Baba,D., Kimura,M., Yamashita,M., Kashiwabara,S. and
 Baba,T.
 TITLE Identification of a hyaluronidase, Hyal5, involved in penetration
 of mouse sperm through cumulus mass
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 102 (50), 18028-18033 (2005)
 PUBMED [16330764](#)
 REFERENCE 2 (residues 1 to 481)
 AUTHORS Zhang,H., Shertok,S., Miller,K., Taylor,L. and Martin-Deleon,P.A.
 TITLE Sperm dysfunction in the Rb(6.16)- and Rb(6.15)-bearing mice
 revisited: involvement of Hyalp1 and Hyal5
 JOURNAL Mol. Reprod. Dev. 72 (3), 404-410 (2005)
 PUBMED [16078272](#)
 COMMENT PROVISIONAL REFSEQ: This record has not yet been subject to final
 NCBI review. The reference sequence was derived from [BC125402.1](#).
 On or before Oct 30, 2006 this sequence version replaced
[gi:20915092](#), [gi:82802536](#), [gi:94378449](#).
 FEATURES Location/Qualifiers
 source 1..481
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /chromosome="6"
 Protein 1..481
 /product="hyaluronoglucosaminidase 4"
 /calculated_mol_wt=54254
 Region 41..373
 /region_name="Glyco_hydro_56"
 /note="Hyaluronidase; pfam01630"
 /db_xref="CDD:89585"
 CDS 1..481
 /gene="Hyal4"
 /coded_by="NM_029848.1:218..1663"
 /db_xref="CCDS:CCDS39441.1"

/db_xref="GeneID:77042"

/db_xref="MGI:1924292"

ORIGIN

```
1  mqlpegqlr  lcvfqpvhlt  sgllilfilk  sisslkparl  pvyqrkpfia  awnaptdlcl
61  ikynltlnlk  vfqmvgsprl  kdrqgnvvif  yanrlgyypw  ytsegvping  glpqntslqv
121 hlkkaaqqdin yyipsenfsg  lavidweywr  pqwarnwntk  diyqrksrtl  isdmkenisa
181 adieysakat  feksakafme  etiklgsksr  pkglwgyyly  pdchnynvya  tnytgsctee
241 evlrnndls  lwnsstalyp  avsirkfsad  sentlhfsrf  rvreslrist  mtsqdyalpv
301 fvytqlgyke  ep11flskqd  listigesaa  lgaagivvwg  dmn1tsseen  ctkvnrfvns
361 dfgsyiinv  raaevcsrhl  cknngrcvrk  twkaahylhl  npasyhieas  edgefivrgr
421 asdtdlavma  enflchcyeg  yegadcremt  easgpsglsl  ssssvitlcl  l1lagyqsiq
481 1
```



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Exhibit E

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Range: from begin to end
 Features: ☒ CDD

☐ 1: [XP_527872](#). Reports PREDICTED: hyalur...[gi:114615742]

[BLink](#), [Conserved Domains](#), [Links](#)

Comment Features Sequence

LOCUS XP_527872 476 aa linear PRI 15-SEP-2006

DEFINITION PREDICTED: hyaluronoglucosaminidase 4 [Pan troglodytes].

ACCESSION XP_527872

VERSION XP_527872.2 GI:114615742

DBSOURCE REFSEQ: accession [XM 527872.2](#)

KEYWORDS .

SOURCE Pan troglodytes (chimpanzee)

ORGANISM [Pan troglodytes](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Haplorrhini; Catarrhini; Hominidae; Pan.

COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW 001238093](#)) using gene prediction method: GNOMON, supported by mRNA and EST evidence.

Also see:

[Documentation of NCBI's Annotation Process](#)

On Sep 15, 2006 this sequence version replaced [gi:55629380](#).

FEATURES

source Location/Qualifiers

1..476

/organism="Pan troglodytes"

/isolate="Yerkes chimp pedigree #C0471 (Clint)"

/db_xref="taxon:9598"

/chromosome="7"

/sex="male"

Protein 1..476

/product="hyaluronoglucosaminidase 4"

/calculated_mol_wt=53658

Region 41..373

/region_name="Glyco_hydro_56"

/note="Hyaluronidase; pfam01630"

/db_xref="CDD:89585"

CDS 1..476

/gene="HYAL4"

/coded_by="XM_527872.2:634..2064"

/db_xref="GeneID:472497"

ORIGIN

```

1 mkvlserqlk lcvvpvhlt swlliffilk sisclkparl piyerkpfia awnaptdqcl
61 ikynlrlnlk mfpvigspla kargqhvtif yvnrlgyypw ytsqgvping glpqnislqv
121 hlekadqdin yyipaedfsg laavidweywr pqwarnwnak dvyrqksrkl isdmgknvsa
181 tdieylakvt feesakafmk etiklgiksr pkgllwggyly pdchnynvya pnytgscped
241 evlrnnelsw lwnssaalyp sigvwkslgd senilrfskf rvhesmrist mtshdyaalp
301 fvytrlgyrd eplfflskqd lvstigesaa lgaagiviwg dmnltsskan ctkvkqfvss

```



361 dlgsyianvt raaevcs1hl crnngrcirk mwnapsylhl npasyhieas edgeftvkgk
421 asdtdlavma dtfschcyqg yegadcreik tadgcsqvsp spgslmtlcl lllasy

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Exhibit F



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☐ 1: [XP_578235](#). Reports PREDICTED: simila...[gi:62647063]

[BLink](#), [Conserved Domains](#), [Links](#)
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LOCUS XP_578235 481 aa linear ROD 22-JUN-2006
 DEFINITION PREDICTED: similar to hyaluronoglucosaminidase 4 [Rattus norvegicus].
 ACCESSION XP_578235
 VERSION XP_578235.1 GI:62647063
 DBSOURCE REFSEQ: accession [XM_578235.1](#)
 KEYWORDS .
 SOURCE Rattus norvegicus (Norway rat)
 ORGANISM [Rattus norvegicus](#)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muroidea; Muridae; Murinae; Rattus.
 COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW_047689](#)) using gene prediction method: GNOMON, supported by mRNA evidence.
 Also see:
[Documentation](#) of NCBI's Annotation Process

FEATURES Location/Qualifiers
 source 1..481
 /organism="Rattus norvegicus"
 /strain="BN/SsNHsdMCW"
 /db_xref="taxon:10116"
 /chromosome="4"
 Protein 1..481
 /product="similar to hyaluronoglucosaminidase 4"
 /calculated_mol_wt=54180
 Region 41..373
 /region_name="Glyco_hydro_56"
 /note="Hyaluronidase; pfam01630"
 /db_xref="CDD:89585"
 CDS 1..481
 /gene="Hyal4"
 /coded_by="XM_578235.1:1..1446"
 /db_xref="GeneID:404783"
 /db_xref="RGD:1303194"

ORIGIN
 1 mqllseggqlr rcvvpvhlt sglliffilk sisslkparl pvyqrkpfia awnaptldcl
 61 ikynlavlntk vfgmvgspri kdrqrnvfif yanklgswpw ytsegvping glpqntslqv
 121 hlekayqdin yyipsenfsg laavidweywr pqwarnwntk diyrqksrtl isdmkenist
 181 adieylakat feksakafme etiklgiksr pkgfwggyly pdchnynfya tnytgscpee
 241 evlrnndlsf lwnsstalyp avsirksfad sentlhfsqf rvreslrist mtshdialpv
 301 fvytrlgyke epllfllskqd listigesaa lgaagivvwg dmnltssaen ctkvnrfvns



```
361 dfgsyvinv taaevcsrhl cknngrcark twkaahylhl npasyhieas adrefvvkgr
421 asdadlaama enflchcyeg yegadcrdmt easgpsgvsv ssssvitlcl ialaghqsiq
481 l
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Range: from to Features: ☒ CDD

☐ 1: [XP_532444](#). Reports PREDICTED: simila...[gi:73975681]

[BLink](#), [Conserved Domains](#), [Links](#)

Comment Features Sequence

LOCUS XP_532444 481 aa linear MAM 30-AUG-2005
 DEFINITION PREDICTED: similar to hyaluronoglucosaminidase 4 isoform 1 [Canis familiaris].

ACCESSION XP_532444
 VERSION XP_532444.2 GI:73975681
 DBSOURCE REFSEQ: accession [XM 532444.2](#)

KEYWORDS

SOURCE Canis lupus familiaris (dog)

ORGANISM [Canis lupus familiaris](#)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Caniformia; Canidae; Canis.

COMMENT MODEL REFSEQ: This record is predicted by automated computational analysis. This record is derived from an annotated genomic sequence ([NW_876258](#)) using gene prediction method: GNOMON, supported by EST evidence.

Also see:

[Documentation](#) of NCBI's Annotation Process

On Aug 30, 2005 this sequence version replaced [gi:57095952](#).

FEATURES

source 1..481
 /organism="Canis lupus familiaris"
 /sub_species="familiaris"
 /db_xref="taxon:9615"
 /chromosome="14"
 /breed="boxer"

Protein 1..481
 /product="similar to hyaluronoglucosaminidase 4 isoform 1"
 /calculated_mol_wt=54487

Region 41..373
 /region_name="Glyco_hydro_56"
 /note="Hyaluronidase; pfam01630"
 /db_xref="CDD:89585"

CDS 1..481
 /gene="LOC475212"
 /coded_by="XM_532444.2:1..1446"
 /db_xref="GeneID:475212"

ORIGIN

1 mkvlsdgqlr lcvvqpihlt swlliffilk sisslkparl piyqrkpfia awnaptdqcl
 61 ikyniglntk mfqvigspla kargqnitif yvnrlgyypw ytsqgvping glpqnislqv
 121 hlekadqdin yyipaedfng laavidweywr pqwarnwntk dvyrqksrkl isdmqenvsa
 181 tdieylakat feesakafmk etielgiksr pkglwgyyly pdchnynvya pnytgscpee
 241 evlrnnelsw lwnssaalyp sigvrksled nenilrfsrf rvheslrist mtshdyalpi

301 fvytrlgyrn eplfflskqd listigesaa lgaagiviwg dmnltsssegn ctkvkqyvss
361 dlghyivnvt raaevcs1hl crsngrcirk vwkapdylhl npasyhieas kdgefivkgk
421 asdmdleale ekfschcyqg yegadcrgtk tadgcsqvfs fssslitlcl lylagyqsir
481 s

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Exhibit H

BLAST Basic Local Alignment Search Tool**Job Title: |cl|791 (1271 letters)**

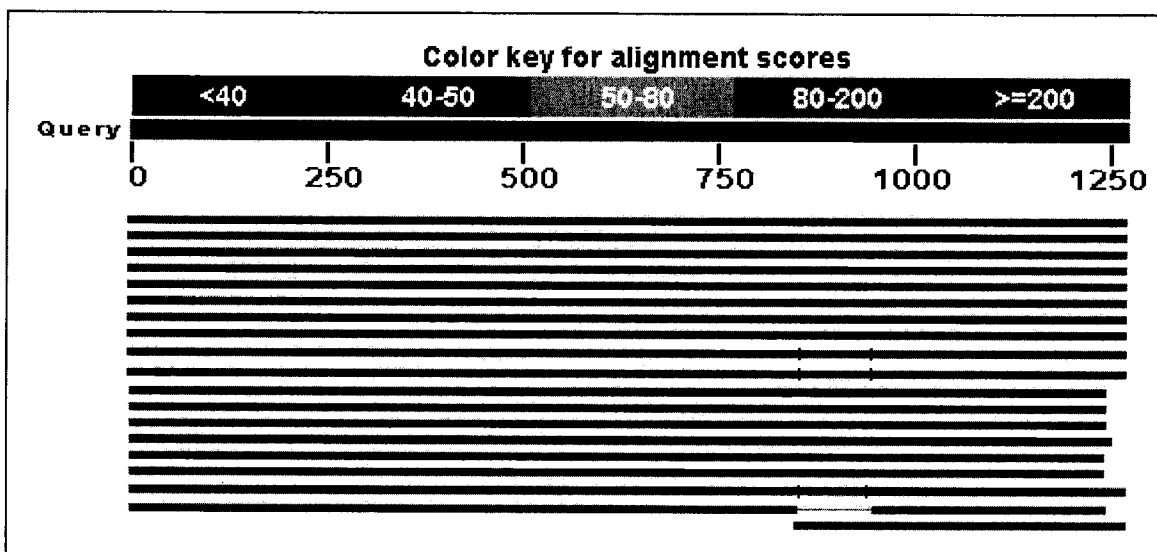
•

Please, try our new design!

BLASTN 2.2.18+

RID: 62JPMG3G013 **Database:** All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environmental samples or phase 0, 1 or 2 HTGS sequences) 6,953,186 sequences; 24,085,767,743 total letters

Query= Length=1271


Distribution of 26 Blast Hits on the Query Sequence

Distance tree of results **NEW**Legend for links to other resources: **U** UniGene **E** GEO **G** Gene **S** Structure **I****Sequences producing significant alignments:**

(Click headers to sort columns)

NM_012269.2	Homo sapiens hyaluronoglucosaminidase 4 (HYAL4), mRNA	2348	2348	100%	0.0	100%	UG
BC104790.1	Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:132450 IMAGE:8143793), complete cds	2342	2342	100%	0.0	99%	UG
BC104788.1	Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:132448 IMAGE:8143791), complete cds	2342	2342	100%	0.0	99%	UG
AF009010.1	Homo sapiens hyaluronidase 4 (HYAL4) mRNA, complete cds	2331	2331	100%	0.0	99%	UE
XM_527872.2	PREDICTED: Pan troglodytes hyaluronoglucosaminidase 4 (HYAL4), mRNA	2287	2287	100%	0.0	99%	G
XM_001086758.1	PREDICTED: Macaca mulatta similar to hyaluronoglucosaminidase 4 (LOC696128), mRNA	2154	2154	100%	0.0	97%	G
XM_001502389.1	PREDICTED: Equus caballus similar to Hyaluronoglucosaminidase 4 (LOC100056514), mRNA	1742	1742	99%	0.0	91%	G
XM_532444.2	PREDICTED: Canis familiaris similar to hyaluronoglucosaminidase 4, transcript variant 1 (LOC475212), mRNA	1659	1659	99%	0.0	90%	UE
AC006029.2	Homo sapiens BAC clone GS1-195F7 from 7q31.2-q32, complete sequence	1578	2359	100%	0.0	100%	
AC197510.3	Pan troglodytes BAC clone CH251-712N23 from chromosome 7, complete sequence	1539	2298	100%	0.0	99%	
BC132096.1	Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:163727 IMAGE:40130373), complete cds	1339	1339	97%	0.0	86%	UG
NM_029848.1	Mus musculus hyaluronoglucosaminidase 4 (Hyal4), mRNA >gb BC125402.1 Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MGC:159105 IMAGE:40129917), complete cds	1339	1339	97%	0.0	86%	UE
AK014599.1	Mus musculus 0 day neonate skin cDNA, RIKEN full-length enriched library, clone:4632428M18 product:similar to HYALURONIDASE 4 [Homo sapiens], full insert sequence	1306	1306	97%	0.0	85%	UE
XM_001370681.1	PREDICTED: Monodelphis domestica similar to Hyaluronoglucosaminidase 4 (LOC100017029), mRNA	1232	1232	98%	0.0	84%	G
XM_001062033.1	PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (Hyal4), mRNA	1212	1212	97%	0.0	84%	G
XM_578235.1	PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (Hyal4), mRNA	1212	1212	97%	0.0	84%	UG
CU467663.10		1136	1632	99%	0.0	90%	

Pig DNA sequence from clone CH242-
113A4 on chromosome 18, complete
sequence

AC130215.3	Mus musculus BAC clone RP23-286E1 from 976 1230 90% 0.0 87%	
	6, complete sequence	
XM_854096.1	PREDICTED: Canis familiaris similar to 475 475 33% 2e- 87%	
	hyaluronoglucosaminidase 4, transcript variant 3 (LOC475212), mRNA	

Alignments

>ref|NM_012269.2| **UG** Homo sapiens hyaluronoglucosaminidase 4 (HYAL4), mRNA
Length=2411

GENE ID: 23553 HYAL4 | hyaluronoglucosaminidase 4 [Homo sapiens]
(10 or fewer PubMed links)

Score = 2348 bits (1271), Expect = 0.0
Identities = 1271/1271 (100%), Gaps = 0/1271 (0%)
Strand=Plus/Plus

Query	1	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	60
Sbjct	739	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	798
Query	61	CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	120
Sbjct	799	CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	858
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	180
Sbjct	859	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	918
Query	181	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	240
Sbjct	919	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	978
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	979	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	1038
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Sbjct	1039	CTGCTGAAGATTTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	1098
Query	361	CCCGGAACTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	1099	CCCGGAACTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	1158
Query	421	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	1159	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	1218
Query	481	GTGCAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	1219	GTGCAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	1278
Query	541	TTTGGGGTTATTATTTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	600
Sbjct	1279	TTTGGGGTTATTATTTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	1338
Query	601	CTGGGTCATGCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	660
Sbjct	1339	CTGGGTCATGCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	1398
Query	661	GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA	720
Sbjct	1399	GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA	1458
Query	721	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	780
Sbjct	1459	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	1518
Query	781	ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	1519	ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1578
Query	841	TTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTG	900

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Sbjct 1579 TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTG 1638
Query 901 CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG 960
Sbjct 1639 CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG 1698
Query 961 TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG 1020
Sbjct 1699 TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG 1758
Query 1021 AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1080
Sbjct 1759 AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1818
Query 1081 CGCCCAGTTACCTTCACTTGAACCTTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG 1140
Sbjct 1819 CGCCCAGTTACCTTCACTTGAACCTTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG 1878
Query 1141 AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1200
Sbjct 1879 AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1938
Query 1201 CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG 1260
Sbjct 1939 CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG 1998
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Sbjct 1999 GCTGCTCTGGG 2009

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>gb|BC104790.1| **UG** Homo sapiens hyaluronoglucosaminidase 4, mRNA (cDNA clone MG IMAGE:8143793), complete cds
Length=1552

GENE ID: 23553 HYAL4 | hyaluronoglucosaminidase 4 [Homo sapiens]
(10 or fewer PubMed links)

Score = 2342 bits (1268), Expect = 0.0
Identities = 1270/1271 (99%), Gaps = 0/1271 (0%)
Strand=Plus/Plus

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Query 1 GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG 60
Sbjct 177 GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG 236
Query 61 CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct 237 CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 296
Query 121 TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA 180
Sbjct 297 TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA 356
Query 181 GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC 240
Sbjct 357 GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC 416
Query 241 AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 300
Sbjct 417 AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 476
Query 301 CTGCTGAAGATTTAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 360
Sbjct 477 CTGCTGAAGATTTAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 536
Query 361 CCCGGAAGTGAAGTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 420
Sbjct 537 CCCGGAAGTGAAGTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 596
Query 421 TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct 597 TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 656

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Query 481  GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC 540
Sbjct 657  GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC 716
Query 541  TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAACTACT 600
Sbjct 717  TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAACTACT 776
Query 601  CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA 660
Sbjct 777  CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA 836
Query 661  GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA 720
Sbjct 837  GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA 896
Query 721  TTTTGCCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC 780
Sbjct 897  TTTTGCCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC 956
Query 781  ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTTAT 840
Sbjct 957  ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTTAT 1016
Query 841  TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAAGTGCTGCCTTGGGAGCTG 900
Sbjct 1017  TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAAGTGCTGCCTTGGGAGCTG 1076
Query 901  CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG 960
Sbjct 1077  CAGGCATTGTTATTTGGGGAGACATGAATTTAACTTCATCCAAGGCCAACTGTACAAAGG 1136
Query 961  TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG 1020
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Query 1021  AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG 1080
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Sbjct 1257  CGCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG 1316
Query 1141  AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1200
Sbjct 1317  AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT 1376
Query 1201  CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG 1260
Sbjct 1377  CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG 1436
Query 1261  GCTGCTCTGGG 1271
Sbjct 1437  GCTGCTCTGGG 1447

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>gb|BC104788.1| **UG** Homo sapiens hyaluronoglucosaminidase 4, mRNA (cdna clone MG IMAGE:8143791), complete cds
Length=1558

GENE ID: 23553 **HYAL4** | hyaluronoglucosaminidase 4 [Homo sapiens]
(10 or fewer PubMed links)

Score = 2342 bits (1268), Expect = 0.0
Identities = 1270/1271 (99%), Gaps = 0/1271 (0%)
Strand=Plus/Plus

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Query 1  GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG 60
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Query 61  CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct 237  CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 296

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Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCAACA	180
Sbjct	297	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCAACA	356
Query	181	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	240
Sbjct	357	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	416
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Sbjct	417	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	476
Query	301	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	477	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	536
Query	361	CCCGGAAGTGGAACTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	537	CCCGGAAGTGGAACTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	596
Query	421	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	597	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	656
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Sbjct	657	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	716
Query	541	TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	600
Sbjct	717	TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	776
Query	601	CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	660
Sbjct	777	CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	836
Query	661	GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA	720
Sbjct	837	GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA	896
Query	721	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	780
Sbjct	897	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	956
Query	781	ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	957	ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1016
Query	841	TTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTG	900
Sbjct	1017	TTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTG	1076
Query	901	CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG	960
Sbjct	1077	CAGGCATTGTTATTTGGGGAGACATGAATTTAACTTCATCCAAGGCCAACTGTACAAAGG	1136
Query	961	TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG	1020
Sbjct	1137	TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG	1196
Query	1021	AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG	1080
Sbjct	1197	AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG	1256
Query	1081	CGCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG	1140
Sbjct	1257	CGCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG	1316
Query	1141	AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT	1200
Sbjct	1317	AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT	1376
Query	1201	CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG	1260
Sbjct	1377	CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATG	1436

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Query 1261 GCTGCTCTGGG 1271
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Sbjct 1437 GCTGCTCTGGG 1447

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>gb|AF009010.1|AF009010 **UEG** Homo sapiens hyaluronidase 4 (HYAL4) mRNA, complet
Length=2414

GENE ID: 23553 HYAL4 | hyaluronoglucosaminidase 4 [Homo sapiens]
(10 or fewer PubMed links)


Score = 2331 bits (1262), Expect = 0.0
Identities = 1268/1271 (99%), Gaps = 0/1271 (0%)
Strand=Plus/Plus

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Query 61     CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct 802    CTCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 861
Query 121    TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA 180
Sbjct 862    TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA 921
Query 181    GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC 240
Sbjct 922    GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC 981
Query 241    AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 300
Sbjct 982    AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 1041
Query 301    CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 360
Sbjct 1042   CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGAGACCACAGTGGG 1101
Query 361    CCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 420
Sbjct 1102   CCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 1161
Query 421    TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct 1162   TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 1221
Query 481    GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC 540
Sbjct 1222   GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC 1281
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Sbjct 1282   TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT 1341
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Sbjct 1342   CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA 1401
Query 661    GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGAGACAGTGAAAACA 720
Sbjct 1402   GCAGTGCTGCTTTATATCCTTCTATCTGTGTCTGGAAATCCCTTGAGACAGTGAAAACA 1461
Query 721    TTTTGCCTTCTCCTCAAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC 780
Sbjct 1462   TTTTGCCTTCTCCTCAAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC 1521
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Sbjct 1522   ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT 1581
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Query	901	CAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGG	960
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Query	961	TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG	1020
Sbjct	1702	TGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCTG	1761
Query	1021	AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG	1080
Sbjct	1762	AGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACG	1821
Query	1081	CGCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG	1140
Sbjct	1822	CGCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGACGGGG	1881
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Sbjct	1882	AGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTTT	1941
Query	1201	CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATG	1260
Sbjct	1942	CCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAGACGGCTGATG	2001
Query	1261	GCTGCTCTGGG	1271
Sbjct	2002	GCTGCTCTGGG	2012


>ref|XM_527872.2|  PREDICTED: Pan troglodytes hyaluronoglucosaminidase 4 (HYAL4 mRNA
Length=2403

GENE ID: 472497 HYAL4 | hyaluronoglucosaminidase 4 [Pan troglodytes]

Score = 2287 bits (1238), Expect = 0.0
Identities = 1261/1272 (99%), Gaps = 2/1272 (0%)
Strand=Plus/Plus

Query	1	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	60
Sbjct	734	GTCTAAAACCTGCTCGACTTCCAATTTATGAAAGGAAACCTTTTATAGCTGCTTGAATG	793
Query	61	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	120
Sbjct	794	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	853
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACATATTTTATGTCAACA	180
Sbjct	854	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAACATGTCACATATTTTATGTCAACA	913
Query	181	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	240
Sbjct	914	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	973
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	974	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	1033
Query	301	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	1034	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	1093
Query	361	CCCGGAAC TGGAAC TCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	1094	CCCGGAAC TGGAAC GCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTGATTTCCGATA	1153
Query	421	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	1154	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	1213
Query	481	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	1214	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	1273

Query	541	TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	600
Sbjct	1274	TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTA-T	1332
Query	601	-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC	659
Sbjct	1333	ACTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC	1392
Query	660	AGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAAC	719
Sbjct	1393	AGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAAC	1452
Query	720	ATTTTGCCTTCTCCAAATTTCTGGGTGCATGAATCCATGAGGATCTCCACCATGACATCT	779
Sbjct	1453	ATTTTGCCTTCTCCAAATTTCTGGGTGCATGAATCCATGAGGATCTCCACCATGACATCT	1512
Query	780	CATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTA	839
Sbjct	1513	CATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTA	1572
Query	840	TTTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCT	899
Sbjct	1573	TTTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCT	1632
Query	900	GCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAG	959
Sbjct	1633	GCAGGCATTGTTATTTGGGGAGACATGAATTTAACTTCATCCAAGGCCAACTGTACAAAG	1692
Query	960	GTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCT	1019
Sbjct	1693	GTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGCT	1752
Query	1020	GAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAAC	1079
Sbjct	1753	GAGGTATGCAGCCTTCACCTCTGCAGGAACAACGGGAGGTGCATAAGGAAGATGTGGAAC	1812
Query	1080	GCGCCAGTTACCTTCACCTTGAACCCGCAAGTTACCACATAGAGGCCTCTGAGGACGGG	1139
Sbjct	1813	GCGCCAGTTACCTTCACCTTGAACCCGCAAGTTACCACATAGAGGCCTCTGAGGACGGG	1872
Query	1140	GAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTT	1199
Sbjct	1873	GAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACATTT	1932
Query	1200	TCCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGAT	1259
Sbjct	1933	TCCTGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGAT	1992
Query	1260	GGCTGCTCTGGG	1271
Sbjct	1993	GGCTGCTCTGGG	2004

>ref|XM_001086758.1|  PREDICTED: Macaca mulatta similar to hyaluronoglucosaminidase 4 (LOC696128), mRNA
Length=1825


GENE ID: 696128 LOC696128 | similar to hyaluronoglucosaminidase 4
[Macaca mulatta]

Score = 2154 bits (1166), Expect = 0.0
Identities = 1238/1273 (97%), Gaps = 4/1273 (0%)
Strand=Plus/Plus

Query	1	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	60
Sbjct	154	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	213
Query	61	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	120
Sbjct	214	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	273
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACATATTTTATGTCAACA	180

Sbjct	274	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACCTATATTTTATGTCAACA	333
Query	181	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	240
Sbjct	334	GATTGGGATACTATCCATGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	393
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	394	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	453
Query	301	CTGCTGAAGATTTTCAGTGGACTTGC'TGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	454	CTGATGAAGATTTTCAGTGGACTTGC'TGTTATAGATTGGGAATATTGGCGACCACAGTGGG	513
Query	361	CCCGGAAC'TGGAAC'T - CAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGAT	419
Sbjct	514	CCCGGAAC'TGGAAC'T - TGCAAAAGACGTCTACAGAAAGAAGTCAAGAAAGCTTATTACCGAT	572
Query	420	ATGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAA	479
Sbjct	573	ATGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCTAAAGTGACCTTTGAAGAA	632
Query	480	AGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGC	539
Sbjct	633	AGCGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGTCGACCCAAAGGT	692
Query	540	CTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAACTAC	599
Sbjct	693	CTTTGGGGTTATTATTTATATCCTGATTGTCACAATTATAATGTTTATGCCCCAAACTA-	751
Query	600	T-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAA	658
Sbjct	752	TACTGGGTCATGCCCAGAAGAGGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAA	811
Query	659	CAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAA	718
Sbjct	812	CAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAA	871
Query	719	CATTTTGCGCTTCTCCAAATTTGGGTGCATGAATCCATGAGGATCTCCACCATGACATC	778
Sbjct	872	CATTTTGCGCTTCTCCCAATTTGGGTACATGAATCCATGAGGATCTCCACCATGACATC	931
Query	779	TCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTT	838
Sbjct	932	TCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTT	991
Query	839	ATTTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGC	898
Sbjct	992	ATTTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGC	1051
Query	899	TGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCA'TCCAAGGCCAACTGTACAAA	958
Sbjct	1052	TGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTTCATCCAAGGCCAACTGTACAAA	1111
Query	959	GGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGC	1018
Sbjct	1112	GGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACCTAGCCAATGTGACCAGAGCTGC	1171
Query	1019	TGAGGTATGCAGCCTTACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAA	1078
Sbjct	1172	TGAGGTATGCAGCTTTACCTCTGCAGGAACAATGGGAGGTGCATAAGGAAGATGTGGAA	1231
Query	1079	CGCGCCCAGTTACCTTACCTTGAACCC'TGCAAGTTACCACATAGAGGCCCTCTGAGGACGG	1138
Sbjct	1232	CTCACCACCTTACCTTACCTTGAACCCCGCAAGTTACCACATAGAGGCCCTCTGAGGATGG	1291
Query	1139	GGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACC'TGGCAGTGATGGCAGATACATT	1198
Sbjct	1292	AGAATTTACTGTGAAAGGAAGAGCATCTGATACAGACC'TGGCAGTGATGGCAGATACATT	1351
Query	1199	TTCTGTTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGA	1258
Sbjct	1352	TTCTGTTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAGTAAAGACGGCTGA	1411
Query	1259	TGGCTGCTCTGGG 1271	

Sbjct 1412 TGGCTGTTCTGGG 1424

>ref|XM_001502389.1|  PREDICTED: Equus caballus similar to Hyaluronoglucosamini
4 (LOC100056514), mRNA
Length=1553

GENE ID: 100056514 LOC100056514 | similar to Hyaluronoglucosaminidase 4
[Equus caballus]

Score = 1742 bits (943), Expect = 0.0
Identities = 1165/1274 (91%), Gaps = 8/1274 (0%)
Strand=Plus/Plus

Query	2	TCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGC	61
Sbjct	173	TCTAAAACCTGCCCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCATGGAATGC	232
Query	62	TCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTGT	121
Sbjct	233	TCCAACAGATCAGTGTGTTGATAAAATATAATATAAGACTAAATCTGAAAATGTTTCAGGT	292
Query	122	GATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACAG	181
Sbjct	293	GATTGGAAGCCCACTGGCCAAGGCTAGAGGGCAAATGTCACTATATTTTATGTCAACAG	352
Query	182	ATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCCACA	241
Sbjct	353	ATTGGGCTACTATCCATGGTATACATCACAGGGGGTTCCTGTTAACGGGGGTCTCCCCCA	412
Query	242	GAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCCC	301
Sbjct	413	GAACATAAGTTTGCAAGTACACCTAGAAAAAGCTGACGAAGATATTAATTACTACATCCC	472
Query	302	TGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGGC	361
Sbjct	473	TGCTGAAGATTTTCAGTGGACTTGCTGTCATAGACTGGGAATACTGGAGACCCCAGTGGGC	532
Query	362	CCGGAAGTGAAGTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATAT	421
Sbjct	533	CCGGAAGTGAAGTCAAAAGATGTCTACAGACAGAAGTCAAGAAAGCTTATTTCTGATAT	592
Query	422	GGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	593	GC-AAGAGAATGTATCAGCTACTGATATTGAATATTTAGCTAAAGCAACCTTTGAAGAAA	651
Query	481	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	652	GTGCAAAAGCTTTTATGAAGGAAACCATCGAATTGGGAATTAAGAGCCGACCCAAAGGCC	711
Query	541	TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	600
Sbjct	712	TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAATGTTTATGACCCAACTA-T	770
Query	601	-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC	659
Sbjct	771	ACTGGGTCATGCCCAGAAGAGGAAGTTTGTAGAAATAATGAGCTCTCTTGGCTCTGGAAC	830
Query	660	AGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAAC	719
Sbjct	831	AGCAGTGCTGCTTTATATCCTTCTATTGGTGTCTAGGAAATCTCTTGGAGACAGCGAAAAC	890
Query	720	ATTTTGCCTTCTC-CAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATC	778
Sbjct	891	ATTTTGCCTTCTCTCGAA-TTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATC	949
Query	779	TCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTT	838
Sbjct	950	CCACGATTATGCTCTGCCTGTATTTGTCTACACAAGACTAGGCTACAGAGACGAACCTTT	1009
Query	839	ATTTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGC	898
Sbjct	1010	ATTTTTCCTTTCTAAGCAAGATCTAATCAGTACCATTGGAGAAAGCGCTGCCTTGGGAGC	1069
Query	899	TGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAA	958

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Sbjct 1070 TGCAGGCTTTGTTATTTGGGGAGACATGAATTTAACTTCATCTGAGGGCAACTGTACAAA 1129
Query 959 GGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGACCAGAGCTGC 1018
Sbjct 1130 GGTGAAGCAGTTTGTGAGCTCTGTTTTAGGGCGCTACATAGTCAACGTGACCCGAGCCGC 1189
Query 1019 TGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAA 1078
Sbjct 1190 CGAGGCGTGCAGCCTCCACCTGTGCAGGAACAACGGGAGATGCCTGAGGAAGGTGTGGAA 1249
Query 1079 CGCGCCC-AGTTACCTTCACCTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGACG 1137
Sbjct 1250 AGCTCCCGA-TTACCTTCATTTGAACCCTGCAAGTTACTACATAGAGGCCTCCGAGGATG 1308
Query 1138 GGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAGATACAT 1197
Sbjct 1309 GAGAATTTATTGTGGAAGGAAAAGCATCTGATACAGACCTGGCCCTGATGGCAGAGAAAT 1368
Query 1198 TTTCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTG 1257
Sbjct 1369 TTTCTGTCAAGTGTATCAGGGATACGAAGGGGCCGATTGCAGAGAAATGAAGACAGCTG 1428
Query 1258 ATGGCTGCTCTGGG 1271
Sbjct 1429 ATGGCTGCTCTGGG 1442

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>ref|XM_532444.2| **UEG** PREDICTED: Canis familiaris similar to hyaluronoglucosaminidase 4, transcript variant 1 (LOC475212), mRNA
Length=1761

GENE ID: 475212 **HYAL4** | hyaluronoglucosaminidase 4 [Canis lupus familiaris]


Score = 1659 bits (898), Expect = 0.0
Identities = 1154/1278 (90%), Gaps = 16/1278 (1%)
Strand=Plus/Plus

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Query 2 TCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGC 61
Sbjct 102 TCTAAACCTGCCCGGCTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGC 161
Query 62 TCCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTGT 121
Sbjct 162 CCCAACGGATCAGTGTGTTGATAAAATACAATATAGGATTAAATTTGAAAATGTTTCAGGT 221
Query 122 GATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACAG 181
Sbjct 222 TATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATATCACTATATTTTATGTCAACAG 281
Query 182 ATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCCACA 241
Sbjct 282 ATTGGGATACTATCCATGGTATACATCACAGGGGGTTCCCATTAATGGGGGTCTCCCCCA 341
Query 242 GAACATAAGTTTACAAGTACATCTGAAAAAGCTGACCAAGATATTAATTATTACATCCC 301
Sbjct 342 GAACATAAGTTTGCAAGTGCATCTAGAAAAAGCTGACCAAGATATTAATTATTACATCCC 401
Query 302 TGCTGAAGATTTTCAAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGGC 361
Sbjct 402 TGCTGAAGATTTCAATGGACTGGCTGTTATAGACTGGGAATACTGGCGACCTCAGTGGGC 461
Query 362 CCGGAAC TGGAAC TCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATAT 421
Sbjct 462 CCGTAAC TGGAAC ACAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTGATTTCTGACAT 521
Query 422 GGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct 522 GC-AAGAGAATGTATCAGCTACTGATATTGAATATTTAGCCAAAGCAACCTTTGAAGAAA 580
Query 481 GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTTGGGAATTAAGAGCCGACCCAAAGG-C 539
Sbjct 581 GTGCAAAAGCTTTTCATGAAGGAAACCATCGAATTTGGGAATTAAGAGTAGACC-AAAGGGC 639
Query 540 CTTTGGGGTTATTATTTATATCTGATTGCCACAATTATAACGTTTATGCCCCAAACTAC 599

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Sbjct	640	CTCTGGGGTTATTATTTATATCCTGATTGCCACAATTATAATGTTTATGCCCCAAATTA-	698
Query	600	T-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAA	658
Sbjct	699	TACTGGGTCATGCCCAGAAGAGGAAGTTTTGAGAAACAATGAGCTCTCTTGGCTCTGGAA	758
Query	659	CAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAA	718
Sbjct	759	TAGTAGTGCTGCTTTATATCCTTCTATTGGTGTGAGAAAATCTCTTGAAGACAATGAAAA	818
Query	719	CATTTTTCGCTTCTC-CAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACAT	777
Sbjct	819	CATTTTTCGCTTCTCGCGA-TTTCGAGTGCATGAATCCCTGAGGATCTCCACCATGACAT	877
Query	778	CTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTT	837
Sbjct	878	CCCATGATTATGCTCTGCCTATATTTGTCTACACAAGGCTAGGCTACAGAAATGAGCCCT	937
Query	838	TATTTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAG	897
Sbjct	938	TATTTTTCTTTCTAAGCAAGATCTAATCAGTACTATTGGAGAAAGTGCTGCCTTGGGAG	997
Query	898	CTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAA	957
Sbjct	998	CTGCAGGCATTGTTATCTGGGGAGACATGAATTTAACTTCATCTGAGGGCAACTGTACAA	1057
Query	958	AGGTGAAGCAGTTTGTGAGTTCTGATTTAGGG-AGCTACATAGCCAATGTGACCAGAGCT	1016
Sbjct	1058	AGGTGAAGCAGTATGTGAGTTCTGACTTAGGACA-CTACATAGTCAATGTGACCAGAGCG	1116
Query	1017	GCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGG	1076
Sbjct	1117	GCTGAGGTGTGCAGCCTTCACCTGTGCAGGAGTAATGGGAGATGCATAAGGAAGGTATGG	1176
Query	1077	AACGCGCCC-AGTTACCTTCACCTGAACCCTGCAAGTTACCACATAGAGGCCTCTGAGGA	1135
Sbjct	1177	AAAGCTCCTGA-TTACCTGCACCTGAACCCTGCAAGTTACCACATAGAGGCCTCCAAGGA	1235
Query	1136	CGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAG-ATA	1194
Sbjct	1236	TGGAGAATTTATTGTGAAAGGAAAAGCATCTGATATGGACCTGGAAGCGTTGG-AGGAGA	1294
Query	1195	CA-TTTTCCTGTCAATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACG	1253
Sbjct	1295	-AGTTTTCTGTCACTGTTATCAGGGATACGAAGGAGCCGACTGTAGAGGAACAAAGACG	1353
Query	1254	GCTGATGGCTGCTCTGGG	1271
Sbjct	1354	GCTGACGGCTGCTCTGGG	1371

>gb|AC006029.2|  Homo sapiens BAC clone GS1-195F7 from 7q31.2-q32, complete seq
Length=143851

Sort alignments for this
E value Score Percen
Query start position

Score = 1578 bits (854), Expect = 0.0
Identities = 854/854 (100%), Gaps = 0/854 (0%)
Strand=Plus/Plus

Query	1	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	60
Sbjct	115835	GTCTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG	1158
Query	61	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	120
Sbjct	115895	CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG	1159
Query	121	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	180
Sbjct	115955	TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACA	1160

Query	181	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	240
Sbjct	116015	GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCAC	1160
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	116075	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	1161
Query	301	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	116135	CTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	1161
Query	361	CCCGBAACTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	116195	CCCGBAACTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	1162
Query	421	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	480
Sbjct	116255	TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA	1163
Query	481	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	540
Sbjct	116315	GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC	1163
Query	541	TTTGGGGTTATTATTTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	600
Sbjct	116375	TTTGGGGTTATTATTTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT	1164
Query	601	CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	660
Sbjct	116435	CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAACA	1164
Query	661	GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA	720
Sbjct	116495	GCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAACA	1165
Query	721	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	780
Sbjct	116555	TTTTGCGCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCTC	1166
Query	781	ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	840
Sbjct	116615	ATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTAT	1166
Query	841	TTTTCTTTCTAAG	854
Sbjct	116675	TTTTCTTTCTAAG	116688

Score = 608 bits (329), Expect = 2e-170
 Identities = 329/329 (100%), Gaps = 0/329 (0%)
 Strand=Plus/Plus

Query	943	AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA	1002
Sbjct	124213	AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA	1242
Query	1003	ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCA	1062
Sbjct	124273	ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCA	1243
Query	1063	TAAGGAAGATGTGGAACGCGCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAG	1122
Sbjct	124333	TAAGGAAGATGTGGAACGCGCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAG	1243
Query	1123	AGGCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG	1182
Sbjct	124393	AGGCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG	1244
Query	1183	TGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG	1242
Sbjct	124453	TGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG	1245
Query	1243	AAATAAGACGGCTGATGGCTGCTCTGGG	1271
Sbjct	124513	AAATAAGACGGCTGATGGCTGCTCTGGG	124541

Score = 172 bits (93), Expect = 3e-39
 Identities = 96/97 (98%), Gaps = 1/97 (1%)
 Strand=Plus/Plus

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Query   849      TCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 908
Sbjct   122217    TCT-AGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 1222

Query   909      GTTATTTGGGGAGACATGAATTTAACTGCATCCAAGG 945
Sbjct   122276    GTTATTTGGGGAGACATGAATTTAACTGCATCCAAGG 122312
  
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>gb|AC197510.3| **D** Pan troglodytes BAC clone CH251-712N23 from chromosome 7, comp
 sequence
 Length=179287

Sort alignments for this
 E value Score Percen
 Query start position

Score = 1539 bits (833), Expect = 0.0
 Identities = 848/855 (99%), Gaps = 2/855 (0%)
 Strand=Plus/Minus

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Query   1      GTCTAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATG 60
Sbjct   87065    GTCTAAACCTGCTCGACTTCCAATTTATGAAAGGAAACCTTTTATAGCTGCTTGAATG 87006

Query   61      CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 120
Sbjct   87005    CTCCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTG 86946

Query   121     TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAAATGTCACTATATTTTATGTCAACA 180
Sbjct   86945    TGATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAACATGTCACTATATTTTATGTCAACA 86886

Query   181     GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCCAC 240
Sbjct   86885    GATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCTCCCAC 86826

Query   241     AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 300
Sbjct   86825    AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC 86766

Query   301     CTGCTGAAGATTTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 360
Sbjct   86765    CTGCTGAAGATTTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG 86706

Query   361     CCCGGAAGTGGAACTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA 420
Sbjct   86705    CCCGGAAGTGGAACTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTGATTTCCGATA 86646

Query   421     TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 480
Sbjct   86645    TGGGAAAGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGAAA 86586

Query   481     GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC 540
Sbjct   86585    GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAGGCC 86526

Query   541     TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTACT 600
Sbjct   86525    TTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAACTA-T 86467

Query   601     -CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC 659
Sbjct   86466    ACTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGAAC 86407

Query   660     AGCAGTGCTGCTTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAAC 719
Sbjct   86406    AGCAGTGCTGCTTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGACAGTGAAAAC 86347
  
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Query 720      ATTTTGCCTTCTCCAAATTTTCGGGTGCATGAATCCATGAGGATCTCCACCATGACATCT 779
Sbjct 86346    ATTTTGCCTTCTCCAAATTTTCGTGTGCATGAATCCATGAGGATCTCCACCATGACATCT 86287
Query 780      CATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTA 839
Sbjct 86286    CATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACCTTTA 86227
Query 840      TTTTTCCTTTCTAAG 854
Sbjct 86226    TTTTTCCTTTCTAAG 86212

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Score = 592 bits (320), Expect = 2e-165
 Identities = 326/329 (99%), Gaps = 0/329 (0%)
 Strand=Plus/Minus

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Query 943      AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA 1002
Sbjct 78688    AGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGAGCTACATAGCCA 78629
Query 1003     ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCA 1062
Sbjct 78628    ATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAACGGGAGGTGCA 78569
Query 1063     TAAGGAAGATGTGGAACGCGCCAGTTACCTTCACCTTGAACCCCTGCAAGTTACCACATAG 1122
Sbjct 78568    TAAGGAAGATGTGGAACGCGCCAGTTACCTTCACCTTGAACCCCGCAAGTTACCACATAG 78509
Query 1123     AGGCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG 1182
Sbjct 78508    AGGCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG 78449
Query 1183     TGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG 1242
Sbjct 78448    TGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG 78389
Query 1243     AAATAAAGACGGCTGATGGCTGCTCTGGG 1271
Sbjct 78388    AAATAAAGACGGCTGATGGCTGCTCTGGG 78360

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Score = 167 bits (90), Expect = 1e-37
 Identities = 95/97 (97%), Gaps = 1/97 (1%)
 Strand=Plus/Minus

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Query 849      TCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 908
Sbjct 80678    TCT-AGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 80620
Query 909      GTTATTTGGGGAGACATGAATTTAACTGCATCCAAGG 945
Sbjct 80619    GTTATTTGGGGAGACATGAATTTAACTTCATCCAAGG 80583

```

>gb|BC132096.1| **UG** Mus musculus hyaluronoglucosaminidase 4, mRNA (cdna clone MG IMAGE:40130373), complete cds
 Length=2088

GENE ID: 77042 **Hyal4** | hyaluronoglucosaminidase 4 [Mus musculus]
 (Over 10 PubMed links)

Score = 1339 bits (725), Expect = 0.0
 Identities = 1089/1262 (86%), Gaps = 36/1262 (2%)
 Strand=Plus/Plus

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Query 3        CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGCT 62
Sbjct 320      CTAAAACCTGCCCAGACTTCCAGTTTATCAAAGGAAACCTTTTATTGCTGCTTGAATGCT 379
Query 63       CCAACAGATCAGTGTTTGTATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG- 120
Sbjct 380      CCAACAGACCTGTGTTTGTATAAAATATAATTTAAGACTGAACCTT-AAAAGTGTTT-CAGA 437
Query 121      TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAAATGTCACATATATTTTATGTCAAC 179

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Sbjct	438	TGGTTGGAAGCCCTC - GGCTCAAAGACAGGGGGCAAATGTTGTTATATTTTATGCCAAC	496
Query	180	AGATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTC - TCCC	238
Sbjct	497	AGATTGGGATATTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTCCC	556
Query	239	ACAGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACAT	298
Sbjct	557	-CAAAACACAAGCTTACAAGTACACCTGAAAAAGCTGCCCAGGATATTAATTATTACAT	615
Query	299	CCCTGCTGAAGATTTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTG	358
Sbjct	616	CCCTTCTGAAAATTTTCACTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAGTG	675
Query	359	GGCCCCGGAAGTGGAACTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGA	418
Sbjct	676	GGCCCCGGAAGTGGAACTCAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTGA	735
Query	419	TATGGGGAA - AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAG	477
Sbjct	736	TAT - GAAAGAGAACATATCTGCTGCTGATATTGAATATTCAGCCAAGGCAACTTTTG - AG	793
Query	478	-AAAGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAA	536
Sbjct	794	AAAAGTGCAAAAGCTTTTCATGGAGGAAACTATCAAATTGGGAAGTAAGAGCAGACCCAAAG	853
Query	537	GGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAAC	596
Sbjct	854	GGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAATGTTTATGCCACAAAC	913
Query	597	TACT - CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTGGCTCTG	655
Sbjct	914	TA - TACTGGGTCATGCCCAGAAGAGGAAGTTTGGAGGAACAATGACCTCTCTGGCTCTG	972
Query	656	GAACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCT - GGAAATCCCTTGAGACAGTG	714
Sbjct	973	GAACAGCAGTACAGCCCTGTATCCTGCTGTGATAT - TAGGAAATCCTTGCAGACAGTG	1031
Query	715	AAAACATTTTGCCTTCTC - CAAATTTGGGTGCATGAATC - CATGAGGATCTCCACCAT	772
Sbjct	1032	AAAACACTTTGCACTTCTCACGA - TTTGGGTGCGTGAATCAC - TGAGGATTTCCACCAT	1089
Query	773	GACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACA - AGGCTAGGG - TACAGAGAT	830
Sbjct	1090	GACATCACAGGATTATGCTCTGCCTGTATTTGTCTACACACAG - CT - GGGCTACAAAGAG	1147
Query	831	GAACCTTTATTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCC	890
Sbjct	1148	GAACCTTTACTTTTCTTTCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCTGCG	1207
Query	891	TTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAAC	950
Sbjct	1208	TTGGGAGCGGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGAGGAGAAC	1267
Query	951	TGTAC - AAAGGTGAAGCAG - TTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGA	1008
Sbjct	1268	TGTACGAAAG - TGAACC - GCTTTGTGAATTCTGATTTTGGCAGCTACATAATCAATGTGA	1325
Query	1009	CCAGAGCTGCTGAGGTATGCAGCCTTACCTCTGCAGGAACAATGGCAGGTGCATAAGGA	1068
Sbjct	1326	CCAGAGCAGCTGAGGTGTGCAGTCGTACCTTTGCAAGAATAATGGGAGGTGTGTACGGA	1385
Query	1069	AGATGTGGAACGC - GCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCC	1127
Sbjct	1386	AGACATGGAAAGCAGCTCA - TTACCTCCATTGAAACCCTGCAAGTTACCACATAGAGGCC	1444
Query	1128	TCTGAGGACGGGGAGTTTACT - GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGAT	1186
Sbjct	1445	TCTGAGGATGGAGAATTCA - TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGTGAT	1503
Query	1187	GGCAGATACATTTTCT - -GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAA	1244
Sbjct	1504	GGCAGAGA - ATTT - CCTATGTCACTGTTATGAGGGATATGAGGGGGCTGACTGTAGAGAA	1561
Query	1245	AT 1246	

Sbjct 1562 AT 1563

>ref|NM_029848.1| **UEG** Mus musculus hyaluronoglucosaminidase 4 (Hyal4), mRNA
 gb|BC125402.1| **UG** Mus musculus hyaluronoglucosaminidase 4, mRNA (cDNA clone MG
 IMAGE:40129917), complete cds
 Length=2088

GENE ID: 77042 Hyal4 | hyaluronoglucosaminidase 4 [Mus musculus]
 (Over 10 PubMed links)

Score = 1339 bits (725), Expect = 0.0
 Identities = 1089/1262 (86%), Gaps = 36/1262 (2%)
 Strand=Plus/Plus

Query	3	CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAAATGCT	62
Sbjct	320	CTAAAACCTGCCCCGACTTCCAGTTTATCAAAGGAAACCTTTTATTGCTGCTTGGAAATGCT	379
Query	63	CCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG-	120
Sbjct	380	CCAACAGACCTGTGTTGATAAAATATAATTTAACTGAACTT-AAAAGTGTTT-CAGA	437
Query	121	TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACCTATATTTTATGTCAAC	179
Sbjct	438	TGGTTGGAAGCCCTC-GGCTCAAAGACAGGGGGCAAATGTTGTTATATTTTATGCCAAC	496
Query	180	AGATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTC-TCCC	238
Sbjct	497	AGATTGGGATATTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTCCC	556
Query	239	ACAGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACAT	298
Sbjct	557	-CAAAACACAAGCTTACAAGTACACCTGAAAAAAGCTGCCCAGGATATTAATTATTACAT	615
Query	299	CCCTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTG	358
Sbjct	616	CCCTTCTGAAAATTTTCAGTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAGTG	675
Query	359	GGCCCCGGAAGTGAAGTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGA	418
Sbjct	676	GGCCCCGGAAGTGAACACAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTGA	735
Query	419	TATGGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAG	477
Sbjct	736	TAT-GAAAGAGAACATATCTGCTGCTGATATTGAATATTCAGCCAAGGCAACTTTTG-AG	793
Query	478	-AAAGTGCAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAA	536
Sbjct	794	AAAAGTGCAAAGCTTTTCATGGAGGAACTATCAAATTGGGAAGTAAGAGCAGACCCAAAG	853
Query	537	GGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAAC	596
Sbjct	854	GGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAATGTTTATGCCACAAC	913
Query	597	TACT-CTGGGTCATGCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTG	655
Sbjct	914	TA-TACTGGGTCATGCCAGAAGAGGAAGTTTTGAGGAACAATGACCTCTCTTGGCTCTG	972
Query	656	GAACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGGAGACAGTG	714
Sbjct	973	GAACAGCAGTACAGCCCTGTATCCTGCTGTCACTAT-TAGGAAATCCTTTGCAGACAGTG	1031
Query	715	AAAACATTTTTCGCTTCTC-CAAATTTTCGGGTGCATGAATC-CATGAGGATCTCCACCAT	772
Sbjct	1032	AAAACACTTTTGCATTTCTCAGCA-TTTCGGGTGCGTGAATCAC-TGAGGATTTCCACCAT	1089
Query	773	GACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACA-AGGCTAGGG-TACAGAGAT	830
Sbjct	1090	GACATCACAGGATTATGCTCTGCCTGTATTTGTCTACACACAG-CT-GGGCTACAAAGAG	1147
Query	831	GAACCTTTTATTTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCC	890

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Sbjct  1148  GAACCTTTACTTTTCTTTCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCTGCG 1207
Query  891  TTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAAC 950
Sbjct  1208  TTGGGAGCGGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGAGGAGAAC 1267
Query  951  TGTAC-AAAGGTGAAGCAG-TTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGTGA 1008
Sbjct  1268  TGTACGAAAG-TGAACC-GCTTTGTGAATTCTGATTTTGGCAGCTACATAATCAATGTGA 1325
Query  1009  CCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGA 1068
Sbjct  1326  CCAGAGCAGCTGAGGTGTGCAGTCGTCACTTTGCAAGAATAATGGGAGGTGTGTACGGA 1385
Query  1069  AGATGTGGAACGC-GCCCAGTTACCTTCACCTGAACCTTGCAAGTTACCACATAGAGGCC 1127
Sbjct  1386  AGACATGGAAAGCAGCTCA-TTACCTCCATTTGAACCTTGCAAGTTACCACATAGAGGCC 1444
Query  1128  TCTGAGGACGGGGAGTTTACT-GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGAT 1186
Sbjct  1445  TCTGAGGATGGAGAATTCA-TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGTGAT 1503
Query  1187  GGCAGATACATTTTCCT--GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAA 1244
Sbjct  1504  GGCAGAGA-ATTT-CCTATGTCACTGTTATGAGGGATATGAGGGGGCTGACTGTAGAGAA 1561
Query  1245  AT 1246
Sbjct  1562  AT 1563

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>dbj|AK014599.1| **UEG** Mus musculus 0 day neonate skin cDNA, RIKEN full-length e library, clone:4632428M18 product:similar to HYALURONIDASE 4 [Homo sapiens], full insert sequence
Length=3255

GENE ID: 77042 Hyal4 | hyaluronoglucosaminidase 4 [Mus musculus]
(Over 10 PubMed links)

Score = 1306 bits (707), Expect = 0.0
Identities = 1085/1264 (85%), Gaps = 40/1264 (3%)
Strand=Plus/Plus

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Query  3  CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAATGCT 62
Sbjct  343  CTAAAACCTGCCCCGACTTCCAGTTTATCAAAGGAAACCTTTTATTGCTGCTTGGAATGCT 402
Query  63  CCAACAGATCAGTGTTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG- 120
Sbjct  403  CCAACAGACCTGTGTTTGATAAAATATAATTTAAGACTGAACTT-AAAAGTGTTT-CAGA 460
Query  121  TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAAC 179
Sbjct  461  TGGTTGGAAGCCCTC-GGCTCAAAGACAGGGGGCAAATGTTGTTATATTTTATGCCAAC 519
Query  180  AGATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTC-TCCC 238
Sbjct  520  AGATTGGGATATTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTCCC 579
Query  239  ACAGAACATAAGTTTACAAGTACATCTGGAAA-AAGCTGACCAAGATATTAATTATTACA 297
Sbjct  580  -CAAAACACAAGCTTACAAGTACACCT-GAAAGGGGCTGGCCAGGATATTAATTATTACA 637
Query  298  TCCCTGCTGAAGATTTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGT 357
Sbjct  638  TCCCTTCTGAAAATTTCACTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCCACAGT 697
Query  358  GGGCCCGGAACCTGGAACCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCG 417
Sbjct  698  GGGCCCGGAACCTGGAACCAAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTG 757
Query  418  ATATGGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAA 476
Sbjct  758  ATAT-GAAAGAGAACATATCTGCTGCTGATATTGAATATTCAGCCAAGGCAACTTTTG-A 815

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Query 477 G-AAAGTGCAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAA 535
Sbjct 816 GAAAAGTGCAAAGCTTTTCATGGAGGAAACATCAAATTGGGAAGTAAGAGCAGACCCAA 875
Query 536 AGGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAA 595
Sbjct 876 GGGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAATGTTTATGCCACAAA 935
Query 596 CTACT-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCT 654
Sbjct 936 CTA-TACTGGGTCATGCCCAGAAGAGGAAGTTTGGAGGAACAATGACCTCTCTTGGCTCT 994
Query 655 GGAACAGCAGTGCTGCTTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGGAGACAGT 713
Sbjct 995 GGAACAGCAGTACAGCCCTGTATCCTGCTGTCTAGTAT-TAGGAAATCCCTTGCAGACAGT 1053
Query 714 GAAACACTTTTGCCTTCTC-CAAAATTCGGGTGCATGAATC-CATGAGGATCTCCACCA 771
Sbjct 1054 GAAACACTTTGCACTTCTCACGA-TTTCGGGTGCGTGAATCAC-TGAGGATTTCCACCA 1111
Query 772 TGACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACA-AGGCTAGGG-TACAGAGA 829
Sbjct 1112 TGACATCACAGGATTATGCTCTGCCTGTATTTGTCTACACACAG-CT-GGGCTACAAAGA 1169
Query 830 TGAACCTTTATTTTCC-TTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAAGTGCTG 888
Sbjct 1170 GGAACCTTTACTTTTCCCTTT-TAAGCAAGATCTAATTAGTACCATAGGAGAAAAGTGCTG 1228
Query 889 CCTTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCA 948
Sbjct 1229 CGTTGGGAGCGGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGAGGAGA 1288
Query 949 ACTGTAC-AAAGGTGAAGCAG-TTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGT 1006
Sbjct 1289 ACTGTACGAAAG-TGAACC-GCTTTGTGAATTCTGATTTTGGCAGCTACATAATCAATGT 1346
Query 1007 GACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAG 1066
Sbjct 1347 GACCAGAGCAGCTGAGGTGTCCAGTCGTCACCTTTGCAAGAATAATGGGAGGTGTGTACG 1406
Query 1067 GAAGATGTGGAACGC-GCCAGTTACCTTCACCTTGAACCCTGCAAGTTACCACATAGAGG 1125
Sbjct 1407 GAAGACATGGAAAGCAGCTCA-TTACCTCCATTTGAACCCTGCAAGTTACCACATAGAGG 1465
Query 1126 CCTCTGAGGACGGGGAGTTTACT-GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTG 1184
Sbjct 1466 CCTCTGAGGATGGAGAATTCA-TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGTG 1524
Query 1185 ATGGCAGATACATTTTCCCT--GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAG 1242
Sbjct 1525 ATGGCAGAGA-ATTT-CCTATGTCACTGTTATGAGGGATATGAGGGGGCTGACTGTAGAG 1582
Query 1243 AAAT 1246
Sbjct 1583 AAAT 1586

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>ref|XM_001370681.1|  PREDICTED: Monodelphis domestica similar to Hyaluronogluc
4 (LOC100017029), mRNA
Length=1446

GENE ID: 100017029 LOC100017029 | similar to Hyaluronoglucosaminidase 4
[Monodelphis domestica]

Score = 1232 bits (667), Expect = 0.0
Identities = 1067/1261 (84%), Gaps = 24/1261 (1%)
Strand=Plus/Plus

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Query 4 TAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGCTC 63
Sbjct 104 TAAAACCTGCACAACCTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGCTC 163
Query 64 CAACAGATCAGTGTTTGATAAAATATAATTTAA-GACTAAATTTGAAAATGTTTC-CTGT 121
Sbjct 164 CAACAGATCAGTGTTCAACAAAGTATAATATAATG-CTGAATTTAAAAATGTTTCACA-T 221

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Query	122	GATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAACAG	181
Sbjct	222	CATTGGCAGTCCATTGGCCAAGGCAAGAGGGCAAATGTTACCATATTTTATGTCAATAG	281
Query	182	ATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCT-CCCAC	240
Sbjct	282	ATTGGGATATTATCCCTGGTATACATCACAAGGAGTTCCTATTAATGGGGGCCTTCCC-C	340
Query	241	AGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCC	300
Sbjct	341	AGAACTTTAGTTTGCAAGCCCATCTGGAAAAAGCTGGCCAAGACATCAATTATTATATTC	400
Query	301	CTGCTGAAGATTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGG	360
Sbjct	401	CAGCTGAGGATTTCACTGGACTTGCTGTCATAGACTGGGAATATTGGAGACCTCAATGGG	460
Query	361	CCCGGAAGTGGAACTCAAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGATA	420
Sbjct	461	CACGGAATTGGAACACAAAAGATGTATACAGGCAGAAGTCAAGAAAGCTAATTTCTGA-A	519
Query	421	TGGGAAAG--AATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAGA	478
Sbjct	520	-GTAAAGTGAACATGTCAGCTAGTGAAATTGAATATTTAGCCAAAATTTCTTTTGAGGA	578
Query	479	AAGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGA-GCCGACCCAAAG	537
Sbjct	579	AAGTGCAAAAGCTTTTCATGAAGGAAACCATCCAGTTGGGAATTC-GAAGTCGCCCCAGGG	637
Query	538	GCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAACT	597
Sbjct	638	GTCTTTGGGGTTACTATTTATATCCTGATTGTCACAATTACAACATTTATGACCAAAATT	697
Query	598	ACTCTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGGA	657
Sbjct	698	ACACTGGTTCATGTCCAGAAGATGAAGTTTTGAGGAACAATGAGCTTTCCTGGCTTTGGA	757
Query	658	ACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGGAGA-CAGTGAA	716
Sbjct	758	ACAGCAGTGCTGCTTTATATCCTTCCATTGGAGTCAAGAAATCTTTTGG-GAACAGTGGA	816
Query	717	AACATTTTGCGCTTCTC-CAAATTTGCGGTGCATGAATCCATGAGGATCTCCACCATGAC	775
Sbjct	817	AACATTTTACGCTTCTCTCAG-TTTAGGGTAAATGAATCAATGCGGATTTCTACCATGAC	875
Query	776	ATCTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGG-TACAGAGATGAAC	834
Sbjct	876	ATCTCATGATTATGCTCTGCCTGTATTTGTCTATACAAGGCT-GGGATACAGAGATGAGC	934
Query	835	CTTTAT-TTTTCCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTG	893
Sbjct	935	CATTATATTTTC-TTTCGAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCTGCCTTG	993
Query	894	GGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGT	953
Sbjct	994	GGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTTCCTCTGAGGGCAACTGT	1053
Query	954	ACAAAGGTGAAGCAGTTTGTGAGTTCCTGATTTAGGGAGCTACATAGCCAATGTGACCAGA	1013
Sbjct	1054	ACAAAGGTGAAACAGTTTGTACTTCTGATCTAGGGAGCTACATCGTTAATGTGACCAA	1113
Query	1014	GCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATG	1073
Sbjct	1114	GCAGCTGAAGTATGCAGCAGACGTCTCTGTAGGAATAATGGAAGATGTGTAAGAAAAATC	1173
Query	1074	TGGAACGCGCCAG-TTACCTTCACTTGAACCCTG-CAAGTTACCACATAGAGGCCTCTG	1131
Sbjct	1174	TGGAAGGCGGC-AGATTATCTCCACCTGAACCCTGACAACTG-CCAGATAGAGGTCTCTG	1231
Query	1132	AGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAG	1191
Sbjct	1232	ATGATGGAGACTTTGCTGTGAAAGGAGAACCTCTGATTCAGACTTGAAAGTGATGGCAG	1291
Query	1192	ATACATTTTCTGTGCTATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGA	1251
Sbjct	1292	AGAGATTTTCTTGTGCTATTGTTATCAGGGATATGGAGGAAAGGATTGCAGGGAAATGAAGA	1351

Query 1252 C 1252
 Sbjct 1352 C 1352

>ref|XM_001062033.1| **G** PREDICTED: Rattus norvegicus hyaluronoglucosaminidase 4 (mRNA)
 Length=1446

GENE ID: 404783 Hyal4 | hyaluronoglucosaminidase 4 [Rattus norvegicus]
 (10 or fewer PubMed links)

Score = 1212 bits (656), Expect = 0.0
 Identities = 1067/1262 (84%), Gaps = 42/1262 (3%)
 Strand=Plus/Plus

Query	3	CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGAATGCT	62
Sbjct	103	CTAAAACCTGCTCGACTTCCAGTTTATCAAAGGAAACCTTTTATAGCTGCTTGGAATGCT	162
Query	63	CCAACAGATCAGTGTGTTGATAAAATATAATTTAAG-ACTAAATTTGAAAA-TGTTTCCTG	120
Sbjct	163	CCAACAGACCTGTGTTGATAAAATATAATTTG-GCAGTGAACCTT-AAAAGTGTTC-A-G	219
Query	121	-TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAA	178
Sbjct	220	ATGGTTGGAAGCCCTC-GGCTCAAAGACAGGAGGCAAATGTTGTTATATTTTATGCCAA	278
Query	179	CAGATTGGGATACT-ATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCT-C	236
Sbjct	279	CAAATTGGGAT-CTTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTC	337
Query	237	CCACAGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTAC	296
Sbjct	338	CC-CAAAACACAAGCTTACAGGTACACCTGGAAAAGGCTTACCAGGATATTAATTATTAC	396
Query	297	ATCCCTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAG	356
Sbjct	397	ATCCCTTCTGAAAATTTTCAGTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAG	456
Query	357	TGGGCCCGGAAGTGAAGTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCC	416
Sbjct	457	TGGGCCCGGAAGTGAACACCAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCT	516
Query	417	GATATG--GGAAAGAATGTATC-AGCTACCGATATTGAATATTTAGCCAAAGTGACCTTT	473
Sbjct	517	GATATGAAGGA--GAACATATCCA-CTGCTGATATTGAATATTTAGCCAAAGCAACTTTT	573
Query	474	GAAGAAA-GTGCAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACC	532
Sbjct	574	GA-GAAAAGTGCAAAGCTTTTCATGGAGGAACTATCAAATTGGGAATTAAGAGCAGACC	632
Query	533	CAAAGGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCC	592
Sbjct	633	CAAGGGCTTTTGGGGTTATTACTTGTATCCTGACTGCCACAATTACAATTTTATGCTAC	692
Query	593	AAACTACT-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGC	651
Sbjct	693	AAACTA-TACCGGTCATGCCCAGAAGAGGAAGTTTGGAGGAACAATGACCTCTCTTGGC	751
Query	652	TCTGGAACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGGAGAC	710
Sbjct	752	TCTGGAACAGCAGTACTGCTCTGTATCCTGCTGTAGTAT-TAGGAAATCCCTTGCAGAC	810
Query	711	AGTGAAAACATTTTGCCTTCTC-CAAATTTCCGGTGCATGAATC-CATGAGGATCTCCA	768
Sbjct	811	AGTGAAAATACTTTGCCTTCTCACA-TTTCGGGTGCGTGAATCAC-TGAGGATCTCTA	868
Query	769	CCATGACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGG-TACAGA	827
Sbjct	869	CTATGACATCACATGATTATGCTCTGCCCGTATTTGTCTACACACGGCT-GGGCTACAA	927
Query	828	GATGAACCTTTATTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCT	887

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Sbjct  928  GAGGAACCTTTGCTTTTCCTTTCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCT  987
Query  888  GCCTTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCC  947
Sbjct  988  GCGTTGGGAGCTGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGCGGAG  1047
Query  948  AACTGTACAAAGGTGAAGCAG-TTTGTGAGTTCCTGATTTAGGGAGCTACATAGCCAATGT  1006
Sbjct  1048  AACTGTACAAAGGTGAACC-GCTTTGTGAACCTCTGATTTTGGTAGCTACGTAATCAATGT  1106
Query  1007  GACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAG  1066
Sbjct  1107  GACCACAGCAGCTGAAGTGTGCAGTCGTCTATCTTTGCAAGAACAATGGGAGGTGTGCACG  1166
Query  1067  GAAGATGTGGAACGC-GCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGG  1125
Sbjct  1167  GAAGACATGGAAAGCAGCTCA-TTACCTCCACTTGAACCCTGCGAGTTACCACATAGAGG  1225
Query  1126  CCTCTG-AGGACGGGGAGTT--TACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG  1182
Sbjct  1226  CCTCTGCAG-ATAGAGAAATTCGTA--GTGAAGGGAAGAGCGTCAGATGCTGACCTAGCCG  1282
Query  1183  TGATGGCAGATACATTTTCC-TGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGA  1241
Sbjct  1283  CCATGGCAGAGA-ATTTTCTATGTCACTGTTATGAGGGCTATGAGGGGGCTGACTGTAGA  1341
Query  1242  GA 1243
Sbjct  1342  GA 1343

```

>ref|**XM_578235.1**| **UG** PREDICTED: *Rattus norvegicus* hyaluronoglucosaminidase 4 (H
mRNA
Length=1446

GENE ID: 404783 Hyal4 | hyaluronoglucosaminidase 4 [*Rattus norvegicus*]
(10 or fewer PubMed links)


Score = 1212 bits (656), Expect = 0.0
Identities = 1067/1262 (84%), Gaps = 42/1262 (3%)
Strand=Plus/Plus

```

Query  3  CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGGAATGCT  62
Sbjct  103  CTAAAACCTGCTCGACTTCCAGTTTATCAAAGGAAACCTTTTATAGCTGCTTGGGAATGCT  162
Query  63  CCAACAGATCAGTGTGTTTGATAAAATATAATTTAAG-ACTAAATTTGAAAA-TGTTTCCTG  120
Sbjct  163  CCAACAGACCTGTGTTTGATAAAATATAATTTG-GCAGTGAACCT-AAAAGTGTTCAG-G  219
Query  121  -TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAA  178
Sbjct  220  ATGTTTGAAGCCCTC-GGCTCAAAGACAGGAGGCAAATGTTGTTATATTTTATGCCAA  278
Query  179  CAGATTGGGATACT-ATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTCT-C  236
Sbjct  279  CAAATTGGGAT-CTTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTC  337
Query  237  CCACAGAACATAAGTTTACAAGTACATCTGGA AAAAGCTGACCAAGATATTAATTATTAC  296
Sbjct  338  CC-CAAAACACAAGCTTACAGGTACACCTGGA AAAAGGCTTACCAGGATATTAATTATTAC  396
Query  297  ATCCCTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAG  356
Sbjct  397  ATCCCTTCTGAAAATTTTCAGTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAG  456
Query  357  TGGGCCCCGGAAGTGAAGTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCC  416
Sbjct  457  TGGGCCCCGGAAGTGAAGTCAAAGATATCTACAGACAGAAGTCAAGAACTCTTATTTCT  516
Query  417  GATATG--GGAAAGAATGTATC-AGCTACCGATATTGAATATTTAGCCAAAGTGACCTTT  473
Sbjct  517  GATATGAAGGA--GAACATATCCA-CTGCTGATATTGAATATTTAGCCAAAGCAACTTTT  573
Query  474  GAAGAAA-GTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACC  532

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Sbjct	574	GA-GAAAAGTGCAAAAGCTTTCATGGAGGAACTATCAAATTGGGAATTAAGAGCAGACC	632
Query	533	CAAAGGCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCC	592
Sbjct	633	CAAGGGCTTTTGGGGTTATTACTTGTATCCTGACTGCCACAATTACAATTTTATGCTAC	692
Query	593	AAACTACT-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGC	651
Sbjct	693	AAACTA-TACCGGGTCATGCCCAGAAGAGGAAGTTTTGAGGAACAATGACCTCTCTTGGC	751
Query	652	TCTGGAACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGAGAGAC	710
Sbjct	752	TCTGGAACAGCAGTACTGCTCTGTATCCTGCTGTTAGTAT-TAGGAAATCCCTTGAGAGAC	810
Query	711	AGTGAAAACATTTTGCCTTCTC-CAAATTTTCGGGTGCATGAATC-CATGAGGATCTCCA	768
Sbjct	811	AGTGAAAATACTTTGCACTTCTCACA-TTTCGGGTGCGTGAATCAC-TGAGGATCTCTA	868
Query	769	CCATGACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGG-TACAGA	827
Sbjct	869	CTATGACATCACATGATTATGCTCTGCCCCTATTTGTCTACACACGGCT-GGGCTACAAA	927
Query	828	GATGAACCTTTATTTTCTTTCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCT	887
Sbjct	928	GAGGAACCTTTGCTTTTCTTTCTAAGCAAGATCTAATTAGTACCATAGGAGAAAGTGCT	987
Query	888	GCCTTGGGAGCTGCAGGCATTGTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCC	947
Sbjct	988	GCGTTGGGAGCTGCAGGCATTGTTGTTTGGGGAGACATGAATTTAACTTCATCTGCGGAG	1047
Query	948	AACTGTACAAAGGTGAAGCAG-TTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATGT	1006
Sbjct	1048	AACTGTACAAAGGTGAACC-GCTTTGTGAAGTCTGATTTTGGTAGCTACGTAATCAATGT	1106
Query	1007	GACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAG	1066
Sbjct	1107	GACCACAGCAGCTGAAGTGTGCAGTCGTCATCTTTGCAAGAACAATGGGAGGTGTGCACG	1166
Query	1067	GAAGATGTGGAACGC-GCCCAGTTACCTTCACCTGAACCCTGCAAGTTACCACATAGAGG	1125
Sbjct	1167	GAAGACATGGAAGCAGCTCA-TTACCTCCACTGAACCCTGCGAGTTACCACATAGAGG	1225
Query	1126	CCTCTG-AGGACGGGGAGTT--TACTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAG	1182
Sbjct	1226	CCTCTGCAG-ATAGAGAATTCGTA--GTGAAGGGAAGAGCGTCAGATGCTGACCTAGCCG	1282
Query	1183	TGATGGCAGATACATTTTCC-TGTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGA	1241
Sbjct	1283	CCATGGCAGAGA-ATTTTCTATGTCACTGTTATGAGGGCTATGAGGGGGCTGACTGTAGA	1341
Query	1242	GA 1243	
Sbjct	1342	GA 1343	

>emb|CU467663.10|  Pig DNA sequence from clone CH242-113A4 on chromosome 18, co
sequence
Length=162313

Sort alignments for this
E value Score Percen
Query start position

Score = 1136 bits (615), Expect = 0.0
Identities = 780/859 (90%), Gaps = 14/859 (1%)
Strand=Plus/Minus

Query	3	CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGGGAATGCT	62
Sbjct	147609	CTAAAACCTGCCCCGACTTCCAGTTTACCAAAGGAAACCTTTTATAGCTGCTTGGGAATGCT	1475
Query	63	CCAACAGATCAGTGTTTTGATAAAATATAATTTAAGACTAAATTTGAAAATGTTTCCTGTG	122
Sbjct	147549	CCAACAGATCAGTGTTTTGATAAAATATAATGTAAGACTAAATTTGAAAATGTTTCAGGTA	1474

Query	123	ATTGGAAGCCCACTGGCCAAGGCCAGGGGGCAAATGTCACATATATTTTATGTCAACAGA	182
Sbjct	147489	ATTGGAAGTCCACTGGCCAGGGCCAGGGGGCAAATGTCACATATATTTTATGTCAACAGA	1474
Query	183	TTGGGATACTATCCGTGGTATACATCACAAGGG-GTCCCCATTAATGGAGGTCTCCACACA	241
Sbjct	147429	CTGGGATACTATCCTTGGTATACAGC-CCAGGGAGTTCCCATTAATGGGGGTCTCCCCCA	1473
Query	242	GAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACATCCC	301
Sbjct	147370	GAACATAAGTCTGCAGGTACATCTGGAAAAAGCAGACCAAGACATTAATTATTACATCCC	1473
Query	302	TGCTGAAGATTTTCACTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTGGGC	361
Sbjct	147310	TTCTGAAGATTTTCACTGGACTTGCTGTTATAGACTGGGAATATTGGCGACCCCAGTGGGC	1472
Query	362	CCGGAACCTGGAACCTCAAAAGATGTTTACAGACAGAAAGTCAAGAAAGCTTATTTCCGATAT	421
Sbjct	147250	CAGGAACCTGGAACACAAAAGATGTCTACAGACAGAAAGTCAAGAAAGCTTATTTCTGAGCT	1471
Query	422	GGGAA-AGAATGTAT-CAGCT-ACCGATATTGAATATTTAGCCAAAGTGACCTTT-GAAG	477
Sbjct	147190	-GCAAGAGAATGTGTCCA--TGGCTGATATTGAATATTTAGCCAAA-ACAACTTTGAGG	1471
Query	478	AAAGTGCAAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAAG	537
Sbjct	147134	AAAGTGCAAAAGCTTTTCATGAAGGAAACCATCGAATTGGGAATTAAGAGCAGACCCAAGG	1470
Query	538	GCCTTTGGGGTTATTATTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAACT	597
Sbjct	147074	GCCTTTGGGGTTACTATTTATATCCTGACTGCCACAATTATAATGTTTATGCCCCAAACT	1470
Query	598	ACT-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTGG	656
Sbjct	147014	A-TACGGGGTCTTGCCCAGAAGAAGAAGTTTTGAGGAACAACGAGCTCTCTTGGCTCTGG	1469
Query	657	AACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCTGGAAATCCCTTGAGACAGTGAA	716
Sbjct	146955	AACAGCAGTGCTGCTTTATATCCTTCTATCAGCGTCAGGAAATCCCTGGGAGACAGTGAA	1468
Query	717	AACATTTTGCCTTCTC-CAAATTTGCGGTGCATGAATCCATGAGGATCTCCACCATGAC	775
Sbjct	146895	AACACTTTGCCTTCTCACA-TTTCGGGTGCATGAATCCATGAGGATCTCCACCGTGAC	1468
Query	776	ATCTCATGATTATGCTCTGCCTGTATTTGTCTACACAAGGCTAGGGTACAGAGATGAACC	835
Sbjct	146836	ATCCCATGGTTATGCTCTGCCTGTGTTTGTCTACACAAGGCTAGGCTACAGAGACCAACC	1467
Query	836	TTTATTTTTCTTTCTAAG	854
Sbjct	146776	TCTGTTTTTTCTTTCTAAG	146758

Score = 381 bits (206), Expect = 4e-102
 Identities = 294/336 (87%), Gaps = 7/336 (2%)
 Strand=Plus/Minus

Query	939	TCCAAGGCCAACTGTACAAAGGTGAAGCAGTTTGTGAGTTCTGATTTAGGGA-GCTACAT	997
Sbjct	140425	TCC-AGGGCAACTGTACAAAGGTGAAGCAGTTTGTAAAGTTCTGACCTA-GGACACTACGT	1403
Query	998	AGCCAATGTGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAG	1057
Sbjct	140367	AGTGAACGTGACCAGAGCCGCTGAGGTGTGCAGCCTTCACCTCTGCAGGAATAACGGGAG	1403
Query	1058	GTGCATAAGGAAGATGTGGAACGCGCCAG-TTACCTTCACCTGAACCCTGCAAGTTACC	1116
Sbjct	140307	ATGCCATAAGGAAGGTGTGGAAGC-TCCGGATTACCTTCACCTGAACCCTGCAAGTTACC	1402
Query	1117	ACATAGAGGCCCTCTGAGGACGGGGAGTTTACTGTGAAAGGAAAAGCATCTGATACAGACC	1176
Sbjct	140248	GCATAGAGGCCCTCTGAGGATGGAGAATTTACTGTGAAAGGAAGAGCATCTGATAGAGACC	1401
Query	1177	TGGCAGTGATGGCAGATACATTTTCTGTCTATTGTTATCAGGGATATGAA-GGAGCTGAT	1235


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Sbjct 140188 TGGCAGTGCTGGTGGAGAGATTCTCCTGTCATTGTTATCAGGGATATGAAGGGA-CTGAT 1401
Query 1236 TGCAGAGAAATAAAGACGGCTGATGGCTGCTCTGGG 1271
Sbjct 140129 TGCAGAGAAATGAAGAGGGCAGATGGCTGCTCTGGG 140094

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Score = 113 bits (61), Expect = 2e-21
 Identities = 83/93 (89%), Gaps = 3/93 (3%)
 Strand=Plus/Minus

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Query 849 TCTAAGCAAGATC-TAGTCAGCACCATAGGAGAAAAGTGCTGCCTTGGGAGCTGCAGGCAT 907
Sbjct 142382 TCT-AGCAAGATCTTA-TCAGTACTATTGGAGAAAAGTGCTGCCTTGGGTGCTGCCGGCTT 1423
Query 908 TGTTATTTGGGGGAGACATGAATTTAACTGCATC 940
Sbjct 142324 TGTTATTTGGGGGAGACATGAATTTAACTTCATC 142292

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>gb|AC130215.3| **D** Mus musculus BAC clone RP23-286E1 from 6, complete sequence
 Length=168515

Sort alignments for this
 E value Score Percen
 Query start position

Score = 976 bits (528), Expect = 0.0
 Identities = 756/864 (87%), Gaps = 24/864 (2%)
 Strand=Plus/Plus

```

Query 3 CTAAAACCTGCTCGACTTCCAATTTATCAAAGGAAACCTTTTATAGCTGCTTGAATGCT 62
Sbjct 106524 CTAAAACCTGCCCAGACTTCCAGTTTATCAAAGGAAACCTTTTATTGCTGCTTGAATGCT 1065
Query 63 CCAACAGATCAGTGTGTTGATAAAATATAATTTAAGACTAAATTTGAAAA-TGTTTCCTG- 120
Sbjct 106584 CCAACAGACCTGTGTTTGATAAAATATAATTTAAGACTGAACTT-AAAAGTGTGTT-CAGA 1066
Query 121 TGATTGGAAGCCCACTGGC-CAAGGCCAGGGGGCAAATGTCACTATATTTTATGTCAAC 179
Sbjct 106642 TGGTTGGAAGCCCTC-GGCTCAAAGACAGGGGGCAAATGTTGTTATATTTTATGCCAAC 1067
Query 180 AGATTGGGATACTATCCGTGGTATACATCACAAGGGGTCCCCATTAATGGAGGTC-TCCC 238
Sbjct 106701 AGATTGGGATATTACCCATGGTATACATCAGAAGGGGTACCCATCAATGGTGGTCTTCCC 1067
Query 239 ACAGAACATAAGTTTACAAGTACATCTGGAAAAAGCTGACCAAGATATTAATTATTACAT 298
Sbjct 106761 -CAAAACACAAGCTTACAAGTACACCTGAAAAAAGCTGCCCAGGATATTAATTATTACAT 1068
Query 299 CCCTGCTGAAGATTTTCAGTGGACTTGCTGTTATAGATTGGGAATATTGGCGACCACAGTG 358
Sbjct 106820 CCCTTCTGAAAATTTTCAGTGGACTTGCTGTTATAGACTGGGAATATTGGCGCCACAGTG 1068
Query 359 GGCCCGGAACCTGGAACCTCAAAGATGTTTACAGACAGAAGTCAAGAAAGCTTATTTCCGA 418
Sbjct 106880 GGCCCGGAACCTGGAACACAAAGGATATCTACAGACAGAAGTCAAGAACTCTTATTTCTGA 1069
Query 419 TATGGGAA-AGAATGTATCAGCTACCGATATTGAATATTTAGCCAAAGTGACCTTTGAAG 477
Sbjct 106940 TAT-GAAAGAGAACATATCTGCTGCTGATATTGAATATTCAGCCAAGGCAACTTTTG-AG 1069
Query 478 -AAAGTGCAAAGCTTTTCATGAAGGAAACCATCAAATTGGGAATTAAGAGCCGACCCAAA 536
Sbjct 106998 AAAAGTGCAAAGCTTTTCATGGAGGAACTATCAAATTGGGAAGTAAGAGCAGACCCAAG 1070
Query 537 GGCCTTTGGGGTTATTATTTTATATCCTGATTGCCACAATTATAACGTTTATGCCCCAAAC 596
Sbjct 107058 GGCCTTTGGGGTTATTATTTTATATCCTGATTGCCACAATTATAATGTTTATGCCACAAC 1071
Query 597 TACT-CTGGGTCATGCCCAGAAGACGAAGTCTTGAGGAACAATGAGCTCTCTTGGCTCTG 655
Sbjct 107118 TA-TACTGGGTCATGCCCAGAAGAGGAAGTTTGGAGGAACAATGACCTCTCTTGGCTCTG 1071

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Query 656      GAACAGCAGTGCTGCTTTATATCCTTCTATCGGTGTCT-GGAAATCCCTTGGAGACAGTG 714
Sbjct 107177   GAACAGCAGTACAGCCCTGTATCCTGCTGTCAGTAT-TAGGAAATCCCTTGCAGACAGTG 1072
Query 715      AAAACATTTTGCCTTCTC-CAAATTTTCGGGTGCATGAATC-CATGAGGATCTCCACCAT 772
Sbjct 107236   AAAACACTTTGCACCTTCTCACGA-TTTCGGGTGCGTGAATCAC-TGAGGATTTCCACCAT 1072
Query 773      GACATCTCATGATTATGCTCTGCCTGTATTTGTCTACACA-AGGCTAGGG-TACAGAGAT 830
Sbjct 107294   GACATCACAGGATTATGCTCTGCCTGTATTTGTCTACACACAG-CT-GGGCTACAAAGAG 1073
Query 831      GAACCTTTATTTTTCCTTTCTAAG 854
Sbjct 107352   GAACCTTTACTTTTTCCTTTCTAAG 107375

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Score = 254 bits (137), Expect = 9e-64
 Identities = 251/305 (82%), Gaps = 12/305 (3%)
 Strand=Plus/Plus

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Query 948      AACTGTAC-AAAGGTGAAGCAG-TTTGTGAGTTCTGATTTAGGGAGCTACATAGCCAATG 1005
Sbjct 116333   AACTGTACGAAA-GTGAA-CCGCTTTGTGAATTCTGATTTTGGCAGCTACATAATCAATG 1163
Query 1006     TGACCAGAGCTGCTGAGGTATGCAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAA 1065
Sbjct 116391   TGACCAGAGCAGCTGAGGTGTGCAGTCGTCACCTTTGCAAGAATAATGGGAGGTGTGTAC 1164
Query 1066     GGAAGATGTGGAACGC-GCCCAGTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAG 1124
Sbjct 116451   GGAAGACATGGAAAGCAGCTCA-TTACCTCCATTTGAACCCTGCAAGTTACCACATAGAG 1165
Query 1125     GCCTCTGAGGACGGGGAGTTTACT-GTGAAAGGAAAAGCATCTGATACAGACCTGGCAGT 1183
Sbjct 116510   GCCTCTGAGGATGGAGAATTCA-TAGTGAGGGGAAGAGCATCAGACACTGACCTAGCTGT 1165
Query 1184     GATGGCAGATACATTTTCTCT--GTCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGA 1241
Sbjct 116569   GATGGCAGAGA-ATTT-CCTATGTCACTGTTATGAGGGATATGAGGGGGCTGACTGTAGA 1166
Query 1242     GAAAT 1246
Sbjct 116627   GAAAT 116631

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>ref|XM_854096.1| **UEG** PREDICTED: Canis familiaris similar to hyaluronoglucosam
 4, transcript variant 3 (LOC475212), mRNA
 Length=1060

GENE ID: 475212 **HYAL4** | hyaluronoglucosaminidase 4 [Canis lupus familiaris]

Score = 475 bits (257), Expect = 2e-130
 Identities = 372/427 (87%), Gaps = 9/427 (2%)
 Strand=Plus/Plus

```

Query 849      TCTAAGCAAGATCTAGTCAGCACCATAGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 908
Sbjct 249      TCT-AGCAAGATCTAATCAGTACTATTGGAGAAAGTGCTGCCTTGGGAGCTGCAGGCATT 307
Query 909      GTTATTTGGGGAGACATGAATTTAACTGCATCCAAGGCCAACTGTACAAAGGTGAAGCAG 968
Sbjct 308      GTTATCTGGGGAGACATGAATTTAACTTCATCTGAGGGCAACTGTACAAAGGTGAAGCAG 367
Query 969      TTTGTGAGTTCTGATTTAGGG-AGCTACATAGCCAATGTGACCAGAGCTGCTGAGGTATG 1027
Sbjct 368      TATGTGAGTTCTGACTTAGGACA-CTACATAGTCAATGTGACCAGAGCGGCTGAGGTGTG 426
Query 1028     CAGCCTTCACCTCTGCAGGAACAATGGCAGGTGCATAAGGAAGATGTGGAACGCGCCC-A 1086
Sbjct 427      CAGCCTTCACCTGTGCAGGAGTAATGGGAGATGCATAAGGAAGGTATGGAAAGCTCCTGA 486
Query 1087     GTTACCTTCACTTGAACCCTGCAAGTTACCACATAGAGGCCCTCTGAGGACGGGGAGTTTA 1146
Sbjct 487      -TTACCTGCACTTGAACCCTGCAAGTTACCACATAGAGGCCCTCCAAGGATGGAGAATTTA 545

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Query 1147 CTGTGAAAGGAAAAGCATCTGATACAGACCTGGCAGTGATGGCAG-ATACA-TTTTCCTG 1204
Sbjct 546 TTGTGAAAGGAAAAGCATCTGATATGGACCTGGAAGCGTTGG-AGGAGA-AGTTTTCTG 603
Query 1205 TCATTGTTATCAGGGATATGAAGGAGCTGATTGCAGAGAAATAAAGACGGCTGATGGCTG 1264
Sbjct 604 TCACTGTTATCAGGGATACGAAGGAGCCGACTGTAGAGGAACAAAGACGGCTGACGGCTG 663
Query 1265 CTCTGGG 1271
Sbjct 664 CTCTGGG 670

```

Database: All GenBank+EMBL+DDBJ+PDB sequences (but no EST, STS, GSS, environment samples or phase 0, 1 or 2 HTGS sequences)

Posted date: Jun 23, 2008 5:48 PM

Number of letters in database: -1,684,036,029

Number of sequences in database: 6,953,186

```

Lambda      K      H
1.33      0.621      1.12

```

Gapped

```

Lambda      K      H
1.33      0.621      1.12

```

Matrix: blastn matrix:1 -2

Gap Penalties: Existence: 0, Extension: 0

Number of Sequences: 6953186

Number of Hits to DB: 3393652

Number of extensions: 1

Number of successful extensions: 1

Number of sequences better than 10: 1

Number of HSP's better than 10 without gapping: 0

Number of HSP's gapped: 1

Number of HSP's successfully gapped: 1

Length of query: 1271

Length of database: 24085767743

Length adjustment: 33

Effective length of query: 1238

Effective length of database: 23856312605

Effective search space: 29534115004990

Effective search space used: 29534115004990

A: 0

X1: 15 (28.8 bits)

X2: 32 (59.1 bits)

X3: 54 (99.7 bits)

S1: 15 (28.8 bits)

S2: 22 (41.7 bits)